

1653

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/331,631A

DATE: 12/28/2000

TIME: 08:00:58

Input Set : A:\CULLN23SEQ.txt

Output Set: N:\CRF3\12282000\I331631A.raw

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ENTERED

4 <110> APPLICANT: Manners, John M.
 5 Marcus, John Paul
 6 Goulter, Kenneth C.
 7 Green, Jodie L.
 9 <120> TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
 12 <130> FILE REFERENCE: CULLN23.001APC
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/331,631A
 C--> 14 <141> CURRENT FILING DATE: 1999-06-21
 14 <150> PRIOR APPLICATION NUMBER: PCT/AU97/00874
 15 <151> PRIOR FILING DATE: 1997-12-22
 17 <150> PRIOR APPLICATION NUMBER: AU PO 4275
 18 <151> PRIOR FILING DATE: 1996-12-20
 20 <160> NUMBER OF SEQ ID NOS: 40
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 666
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Macadamia integrifolia
 29 <400> SEQUENCE: 1
 30 Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
 31 1 5 10 15
 32 Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
 33 20 25 30
 34 Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
 35 35 40 45
 36 Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
 37 50 55 60
 38 Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Glu Asp Pro Gln Thr
 39 65 70 75 80
 40 Glu Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro
 41 85 90 95
 42 Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
 43 100 105 110
 44 Glu Glu Gln Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln
 45 115 120 125
 46 Cys Gln Lys His Cys Gln Arg Arg Glu Thr Glu Pro Arg His Met Gln
 47 130 135 140
 48 Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
 49 145 150 155 160
 50 Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
 51 165 170 175
 52 Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
 53 180 185 190
 54 Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
 55 195 200 205
 56 Gln His Gln Cys Gln Leu Arg Cys Arg Glu Gln Gln Arg Gln His Gly
 57 210 215 220

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58 Arg Gly Gly Asp Met Met Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
59 225 230 235 240
60 Glu Glu Gly Glu Glu Glu Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
61 245 250 255
62 Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
63 260 265 270
64 Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
65 275 280 285
66 Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
67 290 295 300
68 Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Ile Gly Gly Arg Gly
69 305 310 315 320
70 Ala Leu Lys Met Ile His His Asp Asn Arg Glu Ser Tyr Asn Leu Gln
71 325 330 335
72 Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
73 340 345 350
74 Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
75 355 360 365
76 Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
77 370 375 380
78 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
79 385 390 395 400
80 Ala Leu Asn Thr Gln Thr Glu Lys Leu Arg Gly Val Phe Gly Gln Gln
81 405 410 415
82 Arg Glu Gly Val Ile Ile Arg Ala Ser Gln Glu Gln Ile Arg Glu Leu
83 420 425 430
84 Thr Arg Asp Asp Ser Glu Ser Arg His Trp His Ile Arg Arg Gly Gly
85 435 440 445
86 Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
87 450 455 460
88 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
89 465 470 475 480
90 Glu Leu Gln Asp Met Asp Leu Ser Val Phe Ile Ala Asn Val Phe Gln
91 485 490 495
92 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
93 500 505 510
94 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
95 515 520 525
96 Ser Gly Arg His Gly Gly Arg Gly Gly Lys Arg His Glu Glu Glu
97 530 535 540
98 Glu Asp Val His Tyr Glu Gln Val Arg Ala Arg Leu Ser Lys Arg Glu
99 545 550 555 560
100 Ala Ile Val Val Leu Ala Gly His Pro Val Val Phe Val Ser Ser Gly
101 565 570 575
102 Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
103 580 585 590
104 His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
105 595 600 605
106 Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val

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 PATENT APPLICATION: US/09/331,631A DATE: 12/28/2000
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Input Set : A:\CULLN23SEQ.txt
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107 610 615 620
 108 Glu Glu Ser Phe Asn Ser Gln Asp Gln Ser Ile Phe Phe Pro Gly Pro
 109 625 630 635 640
 110 Arg Gln His Gln Gln Gln Ser Pro Arg Ser Thr Lys Gln Gln Gln Pro
 111 645 650 655
 112 Leu Val Ser Ile Leu Asp Phe Val Gly Phe
 113 660 665
 115 <210> SEQ ID NO: 2
 116 <211> LENGTH: 2171
 117 <212> TYPE: DNA
 118 <213> ORGANISM: Macadamia integrifolia
 120 <220> FEATURE:
 121 <221> NAME/KEY: sig_peptide
 122 <222> LOCATION: (1)...(85)
 124 <221> NAME/KEY: mat_peptide
 125 <222> LOCATION: (86)...(1999)
 127 <400> SEQUENCE: 2
 128 atggcgatca atacatcaaa ttatatgtct ctctctcttc tectttcaact ctctctctctg 60
 129 tctacgcacg tgtctctctg tgaagtgaa ttgucagac aggaatatga ggaatgcaca 120
 130 cggcaatgca tgcaglttga gacatcaggc cagatcgtc ggtgtgtgag tcaatgcqal 180
 131 aagagatttg aagagatatt agatttgtct aagtatgata accaagagaa tcttcagacg 240
 132 gaatgccaac aatgcacag gcatgcatg cagcaggaga gtggccacag tcaagcaaca 300
 133 tactgccaac gacgctgcaa ggaatatgt. gaagaagaag aagaatataa ccgacaacgt 360
 134 gatccacagc agcaatacga gcaatgtcag aagcactgcc aaaggcgcca gacagagcca 420
 135 cgtcacatgc aaacatgtca acaacgctgc gagggtgagt atgaaaagaa gaaacgttaa 480
 136 caacaaaaga gatatgaaga gcaacaacgt gaagacgaag agaaatatga agagcgaatg 540
 137 aaggaggaag ataacaacag cgtccacaaa caaagagagt acgaagacta ccagagggcg 600
 138 tgcgaacaac agggagccacg tcaagcagac cagtgcacgc taagatgccc agagcagcag 660
 139 aggcuaacac gccagagtg gcatatgatg aacctcaga ggggagggcg cggcagatuc 720
 140 gaggagggag aagagggaga aagcgacaac cctactact tgcagcaacg aagcttaagt 780
 141 acaaggtlca ggaccgagga aggcacatc tcaattcttg agaacttcta tggtagatcc 840
 142 aagcttctac ggcactataa aaactatcgc ttgtgtctcc tgcaggtcta ccccaacgcc 900
 143 ttctgtctcc ctaccaactt gcatgcatg gccattctct tggctatagg agggagagga 960
 144 gccctcaaaa tgatccacca cgacaacaga gaatcctaca acctcgagtg tggagacgta 1020
 145 atcagaalcc cagctgggac cacattctac ttaatcaaac gagacaacaa cgagagggctc 1080
 146 cacatagcca aqthcttaca gaccatatcc actcctggcc aatacaagga attcttccca 1140
 147 gctggagggc aaaaaccaga gccgtacctc agtaccttca gcaaaagagt tctcagagct 1200
 148 gcgctcaaca caacaacaga gaagctgcgt ggggtgtttg gacagcaaa ggggggagtg 1260
 149 ataattaggg cgtccacaga gcagatcagg gaggttgact gagatgactc agagtcacga 1320
 150 cactggcata taaggagagg tggtagaaca agcaggggac cttacaactc qtlcaacaaa 1380
 151 aagccactgt actccacaaa atacggtcaa gectacgaag tcaaacctga ggactacagg 1440
 152 caactccaag acatggag ct atcgggtttc atagccaacg tcaaccaggg atccatgatg 1500
 153 ggtcctctct tcaacactag gtctacaaa gtggtagtgg tggctagtgg agagggcagat 1560
 154 gtggaaalgg catgccctca ctctgtcggg agacacggcg gccgcgylgg agggaaaagg 1620
 155 catgaggagg aagaggatgt gcactatgag caggttagag caggtttgtc gaagagagag 1680
 156 gccattgttg ttctggcagc tcatcccgtc gtcttctgt catccggaaa cgaagacrtg 1740
 157 ctgctttttg catttggaat caatgcccac aacaaccacg agaacttctc cggcgggaga 1800
 158 gagaggaacg tgcctgcagc qatagagcca caggcaatgg agctagcgtt tgcggctcca 1860
 159 aggaagagag tagaagagtc atttaacagc caggaccagt ctatcttctt tctggggccc 1920

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TECH CENTER 1600, 2900

RAW SEQUENCE LISTING DATE: 12/28/2000
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Input Set : A:\CULLN23SEQ.txt
 Output Set: N:\CRF3\12282000\I331631A.raw

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160 aggcagcacc agcaacagtc gccccgctcc accaagcaac aacagccctct cgtctccatt 1980
161 ctggacttcg ctggttctta aagttccaca aaaaagagtg tggtatglag tataggttag 2040
162 tagctccetg ctggtgttat gaaagtqgtg aagagactaug acgctaaatc cctaaagtaac 2100
163 taacctggcg agcttgctgt tatgcaaata aagaaggaaca gctttccaac tttaaaaaaa 2160
164 aaaaaaaaaa a 2171
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 666
168 <212> TYPE: PRP
169 <213> ORGANISM: Macadamia integrifolia
171 <220> FEATURE:
173 <221> NAME/KEY: SIGNAL
175 <222> LOCATION: (1)...(28)
177 <221> NAME/KEY: PEPTIDE
179 <222> LOCATION: (29)...(666)
181 <400> SEQUENCE: 3
183 Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
184 1 5 10 15
185 Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
186 20 25 30
187 Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
188 35 40 45
189 Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
190 50 55 60
191 Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Asp Asp Pro Gln Thr
192 65 70 75 80
193 Asp Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro
194 85 90 95
195 Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
196 100 105 110
197 Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln
198 115 120 125
199 Cys Gln Glu Arg Cys Gln Arg His Glu Thr Gln Pro Arg His Met Gln
200 130 135 140
201 Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
202 145 150 155 160
203 Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
204 165 170 175
205 Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
206 180 185 190
207 Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
208 195 200 205
209 Gln Tyr Gln Cys Gln Arg Arg Cys Arg Glu Gln Gln Arg Gln His Gly
210 210 215 220
211 Arg Gly Gly Asp Leu Ile Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
212 225 230 235 240
213 Glu Glu Gly Glu Glu Lys Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
214 245 250 255
215 Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
216 260 265 270

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```

213 Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
214      275      280      295
215 Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
216      290      295      300
217 Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Thr Gly Gly Arg Gly
218      305      310      315      320
219 Ala Leu Lys Met Ile His Arg Asp Asn Arg Glu Ser Tyr Asn Leu Glu
220      325      330      335
221 Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
222      340      345      350
223 Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
224      355      360      365
225 Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
226      370      375      380
227 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
228      385      390      395      400
229 Ala Leu Asn Thr Gln Ala Glu Arg Leu Arg Gly Val Leu Gly Gln Gln
230      405      410      415
231 Arg Glu Gly Val Ile Ile Ser Ala Ser Gln Glu Gln Ile Arg Glu Leu
232      420      425      430
233 Thr Arg Asp Asp Ser Glu Ser Arg Arg Trp His Ile Arg Arg Gly Gly
234      435      440      445
235 Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
236      450      455      460
237 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
238      465      470      475      480
239 Gln Leu Glu Asp Met Asp Val Ser Val Phe Ile Ala Asn Ile Thr Gln
240      485      490      495
241 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
242      500      505      510
243 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
244      515      520      525
245 Ser Gly Arg His Gly Gly Arg Arg Gly Gly Lys Arg His Glu Glu Glu
246      530      535      540
247 Glu Asp Val His Tyr Glu Gln Val Lys Ala Arg Leu Ser Lys Arg Glu
248      545      550      555      560
249 Ala Ile Val Val Pro Val Gly His Pro Val Val Phe Val Ser Ser Gly
250      565      570      575
251 Asn Glu Asn Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
252      580      585      590
253 His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
254      595      600      605
255 Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
256      610      615      620
257 Glu Glu Leu Phe Asn Ser Gln Asp Glu Ser Ile Phe Phe Pro Gly Pro
258      625      630      635      640
259 Arg Gln His Gln Gln Ser Ser Arg Ser Thr Lys Gln Gln Gln Pro
260      645      650      655
261 Leu Val Ser Ile Leu Asp Phe Val Gly Phe

```

PJI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 12/28/2000

PATENT APPLICATION: US/09/331,631A

TIME: 08:00:59

Input Set : A:\CULLN23SEQ.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
 L:1238 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
 L:1238 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
 L:1238 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
 L:1240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
 L:1240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
 M:340 Repeated in SeqNo=31
 L:1253 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
 L:1253 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
 L:1253 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
 L:1255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
 L:1255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
 M:340 Repeated in SeqNo=32
 L:1268 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
 L:1268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
 L:1268 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
 L:1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
 L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
 M:340 Repeated in SeqNo=33
 L:1284 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
 L:1284 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
 L:1284 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
 L:1286 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
 L:1286 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
 M:340 Repeated in SeqNo=34
 L:1300 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
 L:1300 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
 L:1300 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
 L:1302 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
 L:1302 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
 M:340 Repeated in SeqNo=35
 L:1316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
 L:1316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
 L:1316 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
 L:1318 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
 L:1318 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
 M:340 Repeated in SeqNo=36
 L:1331 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:37
 L:1331 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
 L:1331 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
 L:1333 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:37
 L:1333 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
 M:340 Repeated in SeqNo=37
 L:1346 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
 L:1346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
 L:1346 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38

VERIFICATION SUMMARY DATE: 12/28/2000
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Input Set : A:\CULLN23SEQ.txt
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L:1348 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:1348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:1361 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:39
L:1361 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
L:1361 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
L:1363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:39
L:1363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:1376 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:1376 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:1376 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40